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RAW SEQUENCE LISTING

DATE: 09/12/2002

PATENT APPLICATION: US/10/029,359A

TIME: 12:28:12

Input Set : A:\10806-156.ST25.txt

Output Set: N:\CRF4\09122002\J029359A.raw

3 <110> APPLICANT: Attersand, Anneli
 5 <120> TITLE OF INVENTION: Protein Cluster II
 7 <130> FILE REFERENCE: 10806-156
 9 <140> CURRENT APPLICATION NUMBER: 10/029,359A
 C--> 10 <141> CURRENT FILING DATE: 2002-08-30
 12 <160> NUMBER OF SEQ ID NOS: 6
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 299
 18 <212> TYPE: DNA
 19 <213> ORGANISM: HUMAN
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 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (21)..(299)
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 32 aaa tcc tgg ctg aat ttt tta acc ttc ctc tat gga tcg gca ata ggg 101
 33 Lys Ser Trp Leu Asn Phe Leu Thr Phe Leu Tyr Gly Ser Ala Ile Gly
 34 15 20 25
 36 ttt att tta ttt tct cag cta ctt agt att ttg ttg gga gaa gag ggt 149
 37 Phe Ile Leu Phe Ser Gln Leu Leu Ser Ile Leu Leu Gly Glu Glu Gly
 38 30 35 40
 40 gac acc cag act aat gtt ctt cat aat gat cct cat gcg agg cat tca 197
 41 Asp Thr Gln Thr Asn Val Leu His Asn Asp Pro His Ala Arg His Ser
 42 45 50 55
 44 gat gat aat gga cag aat cat cta gga gga caa atg aac ttc aat gca 245
 45 Asp Asp Asn Gly Gln Asn His Leu Gly Gly Gln Met Asn Phe Asn Ala
 46 60 65 70 75
 48 gat tct agc caa cgt aaa gat gag aac aca gaa atc gct gaa aac ctc 293
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 50 80 85 90
 52 tat tag 299
 53 Tyr
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 59 <212> TYPE: PRT
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72 Gln Leu Leu Ser Ile Leu Leu Gly Glu Glu Gly Asp Thr Gln Thr Asn
73          35          40          45
76 Val Leu His Asn Asp Pro His Ala Arg His Ser Asp Asp Asn Gly Gln
77          50          55          60
80 Asn His Leu Gly Gly Gln Met Asn Phe Asn Ala Asp Ser Ser Gln Arg
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101                                     Asn
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104 aca ggt gtc act gac aaa ctc tat caa aag atg aaa att ctt tgc tgg          105
105 Thr Gly Val Thr Asp Lys Leu Tyr Gln Lys Met Lys Ile Leu Cys Trp
106          5          10          15
108 att atg aca gga cct caa aat cta gaa aaa aag atc aga cgc atc aga          153
109 Ile Met Thr Gly Pro Gln Asn Leu Glu Lys Lys Ile Arg Arg Ile Arg
110          20          25          30
112 gat aca tgg gcc cag ggt tgc aat aaa gcg ttg ttt atg agc tca aaa          201
113 Asp Thr Trp Ala Gln Gly Cys Asn Lys Ala Leu Phe Met Ser Ser Lys
114          35          40          45
116 gaa aat aaa gac ttc tct act gtg gga tta cac acc aaa gaa gac aga          249
117 Glu Asn Lys Asp Phe Ser Thr Val Gly Leu His Thr Lys Glu Asp Arg
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120 aac caa ctg tcc tgg aaa ata gtt aaa gct ttt cta tat gct cat gac          297
121 Asn Gln Leu Ser Trp Lys Ile Val Lys Ala Phe Leu Tyr Ala His Asp
122          70          75          80
124 cat tat ctg gaa tac atg gat tgg ttc atg aaa gca gat gat gat ata          345
125 His Tyr Leu Glu Tyr Met Asp Trp Phe Met Lys Ala Asp Asp Asp Ile
126          85          90          95
128 tgt ata tat atc aca ttg gac aac ttg aaa tgg ctt ctc aca aac tat          393
129 Cys Ile Tyr Ile Thr Leu Asp Asn Leu Lys Trp Leu Leu Thr Asn Tyr
130          100          105          110
132 aac cct gat gaa tcc act tac ttt ggg aaa aga ttt aag cac tgc aga          441
133 Asn Pro Asp Glu Ser Thr Tyr Phe Gly Lys Arg Phe Lys His Cys Arg
134          115          120          125
136 aaa cag gac tac atg act gga gga gca gga tat gta ctg agc aaa gaa          489
137 Lys Gln Asp Tyr Met Thr Gly Gly Ala Gly Tyr Val Leu Ser Lys Glu
138 130          135          140          145

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152 Trp Ile Met Thr Gly Pro Gln Asn Leu Glu Lys Lys Ile Arg Arg Ile
153 20 25 30
156 Arg Asp Thr Trp Ala Gln Gly Cys Asn Lys Ala Leu Phe Met Ser Ser
157 35 40 45
160 Lys Glu Asn Lys Asp Phe Ser Thr Val Gly Leu His Thr Lys Glu Asp
161 50 55 60
164 Arg Asn Gln Leu Ser Trp Lys Ile Val Lys Ala Phe Leu Tyr Ala His
165 65 70 75 80
168 Asp His Tyr Leu Glu Tyr Met Asp Trp Phe Met Lys Ala Asp Asp Asp
169 85 90 95
172 Ile Cys Ile Tyr Ile Thr Leu Asp Asn Leu Lys Trp Leu Leu Thr Asn
173 100 105 110
176 Tyr Asn Pro Asp Glu Ser Thr Tyr Phe Gly Lys Arg Phe Lys His Cys
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184 Glu
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196 <223> OTHER INFORMATION:
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202 1 5 10 15
204 tct agc caa cat aaa gat gag aac aca gac att gct gaa aac ctc tat 97
205 Ser Ser Gln His Lys Asp Glu Asn Thr Asp Ile Ala Glu Asn Leu Tyr
206 20 25 30
208 cag aaa gtt aga att ctt tgc tgg gtt atg acc ggc cct caa aac cta 145
209 Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly Pro Gln Asn Leu
210 35 40 45
212 gag aaa aag gcc aaa cac gtc aaa gct act tgg gcc cag cgt tgt aac 193
213 Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn
214 50 55 60
216 aaa gtg ttg ttt atg agt tca gaa gaa aat aaa gac ttc cct gct gtg 241
217 Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val
218 65 70 75 80

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222				85						90					95		
224	aaa	gct	ttt	cag	tat	gtt	cat	gaa	cat	tat	tta	caa	gat	gct	gat	tgg	337
225	Lys	Ala	Phe	Gln	Tyr	Val	His	Glu	His	Tyr	Leu	Gln	Asp	Ala	Asp	Trp	
226				100						105					110		
228	ttt	ttg	aaa	gca	gat	gat	gac	acg	tat	gtc	ata	cta	gac	aat	ttg	agg	385
229	Phe	Leu	Lys	Ala	Asp	Asp	Asp	Thr	Tyr	Val	Ile	Leu	Asp	Asn	Leu	Arg	
230				115						120					125		
232	tgg	ctt	ctt	tca	aaa	tac	gac	cct	gaa	gaa	ccc	att	tac	ttt	ggg	aga	433
233	Trp	Leu	Leu	Ser	Lys	Tyr	Asp	Pro	Glu	Glu	Pro	Ile	Tyr	Phe	Gly	Arg	
234		130						135						140			
236	aga	ttt	aag	cct	tat	gta	aag	cag	ggc	tac	atg	agt	gga	gga	gca	gga	481
237	Arg	Phe	Lys	Pro	Tyr	Val	Lys	Gln	Gly	Tyr	Met	Ser	Gly	Gly	Ala	Gly	
238	145					150				155					160		
240	tat	gta	cta	agc	aaa	gaa	gcc	ttg	aaa	aga	ttt	gtt	gat	gca	ttt	aaa	529
241	Tyr	Val	Leu	Ser	Lys	Glu	Ala	Leu	Lys	Arg	Phe	Val	Asp	Ala	Phe	Lys	
242				165						170					175		
244	aca	gac	aag	tgt	aca	cat	agt	tcc	tcc	att	gaa	gac	tta	gca	ctg	ggg	577
245	Thr	Asp	Lys	Cys	Thr	His	Ser	Ser	Ser	Ile	Glu	Asp	Leu	Ala	Leu	Gly	
246				180						185					190		
248	aga	tgc	atg	gaa	att	atg	aat	gta	gaa	gca	gga	gat	tcc	aga	gat	acc	625
249	Arg	Cys	Met	Glu	Ile	Met	Asn	Val	Glu	Ala	Gly	Asp	Ser	Arg	Asp	Thr	
250				195						200					205		
252	att	gga	aaa	gaa	act	ttt	cat	ccc	ttt	gtg	cca	gaa	cac	cat	tta	att	673
253	Ile	Gly	Lys	Glu	Thr	Phe	His	Pro	Phe	Val	Pro	Glu	His	His	Leu	Ile	
254				210						215					220		
256	aaa	ggt	tat	cta	cct	aga	acg	ttt	tgg	tac	tgg	aat	tac	aac	tat	tat	721
257	Lys	Gly	Tyr	Leu	Pro	Arg	Thr	Phe	Trp	Tyr	Trp	Asn	Tyr	Asn	Tyr	Tyr	
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261	Pro	Pro	Val	Glu	Gly	Pro	Gly	Cys	Cys	Ser	Asp	Leu	Ala	Val	Ser	Phe	
262						245					250				255		
264	cac	tat	gtt	gat	tct	aca	acc	atg	tat	gag	tta	gaa	tac	ctc	gtt	tat	817
265	His	Tyr	Val	Asp	Ser	Thr	Thr	Met	Tyr	Glu	Leu	Glu	Tyr	Leu	Val	Tyr	
266				260						265					270		
268	cat	ctt	cgt	cca	tat	ggt	tat	tta	tac	aga	tat	caa	cct	acc	tta	cct	865
269	His	Leu	Arg	Pro	Tyr	Gly	Tyr	Leu	Tyr	Arg	Tyr	Gln	Pro	Thr	Leu	Pro	
270				275						280					285		
272	gaa	cgt	ata	cta	aag	gaa	att	agt	caa	gca	aac	aaa	aat	gaa	gat	aca	913
273	Glu	Arg	Ile	Leu	Lys	Glu	Ile	Ser	Gln	Ala	Asn	Lys	Asn	Glu	Asp	Thr	
274				290						295					300		
276	aaa	gtg	aag	tta	gga	aat	cct	tgaaagaaaa	tcatgaatga	acaaaggtaa							964
277	Lys	Val	Lys	Leu	Gly	Asn	Pro										
278	305									310							
280	tatgtctagc	actgcactga	aaaaggactt	ctgcatttct	gacatagaac	actggaatcc											1024
282	cagtgaggaa	ttctaagtga	acattcctta	tagaaacctt	tcacatgaat	gactataaac											1084
284	tgaagcttta	aatgagctgt	gaagtgtgtt	aaaatgtgtt	ttgatacagt	aatatataaa											1144
286	tatgtctata	tatatgagga	acttgtgttt	tttaaagtgt	ggccaggtag	aggaactaga											1204

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292 aagaaaattt tagaaagaaa tattgttgct cagtgttggt aatatagctc aagaattgag 1384
294 tttatatattg cagtatgcta taaatgatac cccctacca caccacaca cacagttttt 1444
296 gtctaatagaa aatgttgctg tgattattta taattggtag tatttcttcc agaagaagct 1504
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313 20 25 30
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317 35 40 45
320 Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn
321 50 55 60
324 Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val
325 65 70 75 80
328 Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr Trp Lys Thr Ile
329 85 90 95
332 Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Gln Asp Ala Asp Trp
333 100 105 110
336 Phe Leu Lys Ala Asp Asp Asp Thr Tyr Val Ile Leu Asp Asn Leu Arg
337 115 120 125
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341 130 135 140
344 Arg Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser Gly Gly Ala Gly
345 145 150 155 160
348 Tyr Val Leu Ser Lys Glu Ala Leu Lys Arg Phe Val Asp Ala Phe Lys
349 165 170 175
352 Thr Asp Lys Cys Thr His Ser Ser Ser Ile Glu Asp Leu Ala Leu Gly
353 180 185 190
356 Arg Cys Met Glu Ile Met Asn Val Glu Ala Gly Asp Ser Arg Asp Thr
357 195 200 205
360 Ile Gly Lys Glu Thr Phe His Pro Phe Val Pro Glu His His Leu Ile
361 210 215 220
364 Lys Gly Tyr Leu Pro Arg Thr Phe Trp Tyr Trp Asn Tyr Asn Tyr Tyr
365 225 230 235 240
368 Pro Pro Val Glu Gly Pro Gly Cys Cys Ser Asp Leu Ala Val Ser Phe
369 245 250 255
372 His Tyr Val Asp Ser Thr Thr Met Tyr Glu Leu Glu Tyr Leu Val Tyr
373 260 265 270
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